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RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/807,635A

TIME: 11:05:31

Input Set : D:\51158-20011.11 - seq list (txt).txt

Output Set: N:\CRF4\08262004\J807635A.raw

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3 <110> APPLICANT: Daniel E.H. Afar
4     Rene S. Hubert
5     Kahan Leong
6     Arthur B. Raitano
7     Douglas C. Saffran
9 <120> TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
10    IN PROSTATE CANCER
12 <130> FILE REFERENCE: 51158-20011.11
14 <140> CURRENT APPLICATION NUMBER: US 10/807,635A
15 <141> CURRENT FILING DATE: 2004-03-23
17 <150> PRIOR APPLICATION NUMBER: US 10/285,045
18 <151> PRIOR FILING DATE: 2002-10-30
20 <150> PRIOR APPLICATION NUMBER: US 09/547,789
21 <151> PRIOR FILING DATE: 2000-04-12
23 <150> PRIOR APPLICATION NUMBER: 60/128,858
24 <151> PRIOR FILING DATE: 1999-04-12
26 <160> NUMBER OF SEQ ID NOS: 71
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2585
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (4)...(2136)
39 <400> SEQUENCE: 1
40 gcc atg ggg gga aag cag cgg gac gag gat gac gag gcc tac ggg aag      48
41   Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys
42   1           5           10           15
44 cca gtc aaa tac gac ccc tcc ttt cga ggc ccc atc aag aac aga agc      96
45 Pro Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser
46           20           25           30
48 tgc aca gat gtc atc tgc tgc gtc ctc ttc ctg ctc ttc att cta ggt      144
49 Cys Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly
50           35           40           45
52 tac atc gtg gtg ggg att gtg gcc tgg ttg tat gga gac ccc cgg caa      192
53 Tyr Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln
54           50           55           60
56 gtc ctc tac ccc agg aac tct act ggg gcc tac tgt ggc atg ggg gag      240
57 Val Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu
58           65           70           75
60 aac aaa gat aag ccg tat ctc ctg tac ttc aac atc ttc agc tgc atc      288
61 Asn Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile

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62	80		85		90		95	
64	ctg tcc agc aac atc atc tca gtt gct gag aac ggc cta cag tgc ccc	336						
65	Leu Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro							
66			100		105		110	
68	aca ccc cag gtg tgt gtg tcc tcc tgc ccg gag gac cca tgg act gtg	384						
69	Thr Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Val							
70			115		120		125	
72	gga aaa aac gag ttc tca cag act gtt ggg gaa gtc ttc tat aca aaa	432						
73	Gly Lys Asn Glu Phe Ser Gln Thr Val Gly Glu Val Phe Tyr Thr Lys							
74			130		135		140	
76	aac agg aac ttt tgt ctg cca ggg gta ccc tgg aat atg acg gtg atc	480						
77	Asn Arg Asn Phe Cys Leu Pro Gly Val Pro Trp Asn Met Thr Val Ile							
78			145		150		155	
80	aca agc ctg caa cag gaa ctc tgc ccc agt ttc ctc ctc ccc tct gct	528						
81	Thr Ser Leu Gln Gln Glu Leu Cys Pro Ser Phe Leu Leu Pro Ser Ala							
82	160		165		170		175	
84	cca gct ctg ggg cgc tgc ttt cca tgg acc aac gtt act cca ccg gcg	576						
85	Pro Ala Leu Gly Arg Cys Phe Pro Trp Thr Asn Val Thr Pro Pro Ala							
86			180		185		190	
88	ctc cca ggg atc acc aat gac acc acc ata cag cag ggg atc agc ggt	624						
89	Leu Pro Gly Ile Thr Asn Asp Thr Thr Ile Gln Gln Gly Ile Ser Gly							
90			195		200		205	
92	ctt att gac agc ctc aat gcc cga gac atc agt gtt aag atc ttt gaa	672						
93	Leu Ile Asp Ser Leu Asn Ala Arg Asp Ile Ser Val Lys Ile Phe Glu							
94			210		215		220	
96	gat ttt gcc cag tcc tgg tat tgg att ctt gtt gcc ctg ggg gtg gct	720						
97	Asp Phe Ala Gln Ser Trp Tyr Trp Ile Leu Val Ala Leu Gly Val Ala							
98			225		230		235	
100	ctg gtc ttg agc cta ctg ttt atc ttg ctt ctg cgc ctg gtg gct ggg	768						
101	Leu Val Leu Ser Leu Leu Phe Ile Leu Leu Leu Arg Leu Val Ala Gly							
102	240		245		250		255	
104	ccc ctg gtg ctg gtg ctg atc ctg gga gtg ctg ggc gtg ctg gca tac	816						
105	Pro Leu Val Leu Val Leu Ile Leu Gly Val Leu Gly Val Leu Ala Tyr							
106			260		265		270	
108	ggc atc tac tac tgc tgg gag gag tac cga gtg ctg cgg gac aag ggc	864						
109	Gly Ile Tyr Tyr Cys Trp Glu Glu Tyr Arg Val Leu Arg Asp Lys Gly							
110			275		280		285	
112	gcc tcc atc tcc cag ctg ggt ttc acc acc aac ctc agt gcc tac cag	912						
113	Ala Ser Ile Ser Gln Leu Gly Phe Thr Thr Asn Leu Ser Ala Tyr Gln							
114			290		295		300	
116	agc gtg cag gag acc tgg ctg gcc gcc ctg atc gtg ttg gcg gtg ctt	960						
117	Ser Val Gln Glu Thr Trp Leu Ala Ala Leu Ile Val Leu Ala Val Leu							
118			305		310		315	
120	gaa gcc atc ctg ctg ctg atg ctc atc ttc ctg cgg cag cgg att cgt	1008						
121	Glu Ala Ile Leu Leu Leu Met Leu Ile Phe Leu Arg Gln Arg Ile Arg							
122	320		325		330		335	
124	att gcc atc gcc ctc ctg aag gag gcc agc aag gct gtg gga cag atg	1056						
125	Ile Ala Ile Ala Leu Lys Glu Ala Ser Lys Ala Val Gly Gln Met							
126			340		345		350	

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128	atg	tct	acc	atg	ttc	tac	cca	ctg	gtc	acc	ttt	gtc	ctc	ctc	ctc	atc	1104
129	Met	Ser	Thr	Met	Phe	Tyr	Pro	Leu	Val	Thr	Phe	Val	Leu	Leu	Leu	Ile	
130				355					360				365				
132	tgc	att	gcc	tac	tgg	gcc	atg	act	gct	ctg	tac	ctg	gct	aca	tcg	ggg	1152
133	Cys	Ile	Ala	Tyr	Trp	Ala	Met	Thr	Ala	Leu	Tyr	Leu	Ala	Thr	Ser	Gly	
134			370					375					380				
136	caa	ccc	cag	tat	gtg	ctc	tgg	gca	tcc	aac	atc	agc	tcc	ccc	ggc	tgt	1200
137	Gln	Pro	Gln	Tyr	Val	Leu	Trp	Ala	Ser	Asn	Ile	Ser	Ser	Pro	Gly	Cys	
138		385					390					395					
140	gag	aaa	gtg	cca	ata	aat	aca	tca	tgc	aac	ccc	acg	gcc	cac	ctt	gtg	1248
141	Glu	Lys	Val	Pro	Ile	Asn	Thr	Ser	Cys	Asn	Pro	Thr	Ala	His	Leu	Val	
142	400				405					410					415		
144	aac	tcc	tcg	tgc	cca	ggg	ctg	atg	tgc	gtc	ttc	cag	ggc	tac	tca	tcc	1296
145	Asn	Ser	Ser	Cys	Pro	Gly	Leu	Met	Cys	Val	Phe	Gln	Gly	Tyr	Ser	Ser	
146				420						425				430			
148	aaa	ggc	cta	atc	caa	cgt	tct	gtc	ttc	aat	ctg	caa	atc	tat	ggg	gtc	1344
149	Lys	Gly	Leu	Ile	Gln	Arg	Ser	Val	Phe	Asn	Leu	Gln	Ile	Tyr	Gly	Val	
150			435						440					445			
152	ctg	ggg	ctc	ttc	tgg	acc	ctt	aac	tgg	gta	ctg	gcc	ctg	ggc	caa	tgc	1392
153	Leu	Gly	Leu	Phe	Trp	Thr	Leu	Asn	Trp	Val	Leu	Ala	Leu	Gly	Gln	Cys	
154		450					455					460					
156	gtc	ctc	gct	gga	gcc	ttt	gcc	tcc	ttc	tac	tgg	gcc	ttc	cac	aag	ccc	1440
157	Val	Leu	Ala	Gly	Ala	Phe	Ala	Ser	Phe	Tyr	Trp	Ala	Phe	His	Lys	Pro	
158		465				470					475						
160	cag	gac	atc	cct	acc	ttc	ccc	tta	atc	tct	gcc	ttc	atc	cgc	aca	ctc	1488
161	Gln	Asp	Ile	Pro	Thr	Phe	Pro	Leu	Ile	Ser	Ala	Phe	Ile	Arg	Thr	Leu	
162	480				485					490				495			
164	cgt	tac	cac	act	ggg	tca	ttg	gca	ttt	gga	gcc	ctc	atc	ctg	acc	ctt	1536
165	Arg	Tyr	His	Thr	Gly	Ser	Leu	Ala	Phe	Gly	Ala	Leu	Ile	Leu	Thr	Leu	
166			500						505					510			
168	gtg	cag	ata	gcc	cgg	gtc	atc	ttg	gag	tat	att	gac	cac	aag	ctc	aga	1584
169	Val	Gln	Ile	Ala	Arg	Val	Ile	Leu	Glu	Tyr	Ile	Asp	His	Lys	Leu	Arg	
170			515						520					525			
172	gga	gtg	cag	aac	cct	gta	gcc	cgc	tgc	atc	atg	tgc	tgt	ttc	aag	tgc	1632
173	Gly	Val	Gln	Asn	Pro	Val	Ala	Arg	Cys	Ile	Met	Cys	Cys	Phe	Lys	Cys	
174		530					535						540				
176	tgc	ctc	tgg	tgt	ctg	gaa	aaa	ttt	atc	aag	ttc	cta	aac	cgc	aat	gca	1680
177	Cys	Leu	Trp	Cys	Leu	Glu	Lys	Phe	Ile	Lys	Phe	Leu	Asn	Arg	Asn	Ala	
178		545				550					555						
180	tac	atc	atg	atc	gcc	atc	tac	ggg	aag	aat	ttc	tgt	gtc	tca	gcc	aaa	1728
181	Tyr	Ile	Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn	Phe	Cys	Val	Ser	Ala	Lys	
182	560				565					570				575			
184	aat	gcg	ttc	atg	cta	ctc	atg	cga	aac	att	gtc	agg	gtg	gtc	gtc	ctg	1776
185	Asn	Ala	Phe	Met	Leu	Leu	Met	Arg	Asn	Ile	Val	Arg	Val	Val	Val	Leu	
186			580						585					590			
188	gac	aaa	gtc	aca	gac	ctg	ctg	ctg	ttc	ttt	ggg	aag	ctg	ctg	gtg	gtc	1824
189	Asp	Lys	Val	Thr	Asp	Leu	Leu	Leu	Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	
190			595						600				605				
192	gga	ggc	gtg	ggg	gtc	ctg	tcc	ttc	ttt	ttt	ttc	tcc	ggt	cgc	atc	ccg	1872

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193 Gly Gly Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro
194          610          615          620
196 ggg ctg ggt aaa gac ttt aag agc ccc cac ctc aac tat tac tgg ctg      1920
197 Gly Leu Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu
198          625          630          635
200 ccc atc atg acc tcc atc ctg ggg gcc tat gtc atc gcc agc ggc ttc      1968
201 Pro Ile Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe
202 640          645          650          655
204 ttc agc gtt ttc ggc atg tgt gtg gac acg ctc ttc ctc tgc ttc ctg      2016
205 Phe Ser Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu
206          660          665          670
208 gaa gac ctg gag cgg aac aac ggc tcc ctg gac cgg ccc tac tac atg      2064
209 Glu Asp Leu Glu Arg Asn Asn Gly Ser Leu Asp Arg Pro Tyr Tyr Met
210          675          680          685
212 tcc aag agc ctt cta aag att ctg ggc aag aag aac gag gcg ccc ccg      2112
213 Ser Lys Ser Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro
214          690          695          700
216 gac aac aag aag agg aag aag tga cagctccggc cctgatccag gactgcaccc      2166
217 Asp Asn Lys Lys Arg Lys Lys *
218          705          710
220 cacccccacc gtccagccat ccaacctcac ttgccttac aggtctccat tttgtggtaa      2226
221 aaaaaggttt taggccaggc gccgtggctc acgcctgtaa tccaacactt tgagaggctg      2286
222 aggcggggcgg atcacctgag tcaggagttc gagaccagcc tggccaacat ggtgaaacct      2346
223 ccgtctctat taaaaataca aaaattagcc gagagtgggtg gcatgcacct gtcacccag      2406
224 ctactcggga ggctgaggca ggagaatcgc ttgaaccggg gaggcagagg ttgcagtgag      2466
225 ccgagatcgc gccactgcac tccaacctgg gtgacagact ctgtctccaa aacaaaaaaa      2526
226 acaaacaaaa agattttatt aaagatattt tgттаactca gtaaaaaaaaa aaaaaaaaaa      2585
228 <210> SEQ ID NO: 2
229 <211> LENGTH: 710
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 2
234 Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro
235 1          5          10          15
236 Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
237          20          25          30
238 Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr
239          35          40          45
240 Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val
241          50          55          60
242 Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn
243 65          70          75          80
244 Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu
245          85          90          95
246 Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr
247          100          105          110
248 Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Val Gly
249          115          120          125
250 Lys Asn Glu Phe Ser Gln Thr Val Gly Glu Val Phe Tyr Thr Lys Asn

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251      130      135      140
252 Arg Asn Phe Cys Leu Pro Gly Val Pro Trp Asn Met Thr Val Ile Thr
253 145      150      155      160
254 Ser Leu Gln Gln Glu Leu Cys Pro Ser Phe Leu Leu Pro Ser Ala Pro
255      165      170      175
256 Ala Leu Gly Arg Cys Phe Pro Trp Thr Asn Val Thr Pro Pro Ala Leu
257      180      185      190
258 Pro Gly Ile Thr Asn Asp Thr Thr Ile Gln Gln Gly Ile Ser Gly Leu
259      195      200      205
260 Ile Asp Ser Leu Asn Ala Arg Asp Ile Ser Val Lys Ile Phe Glu Asp
261      210      215      220
262 Phe Ala Gln Ser Trp Tyr Trp Ile Leu Val Ala Leu Gly Val Ala Leu
263 225      230      235      240
264 Val Leu Ser Leu Leu Phe Ile Leu Leu Leu Arg Leu Val Ala Gly Pro
265      245      250      255
266 Leu Val Leu Val Leu Ile Leu Gly Val Leu Gly Val Leu Ala Tyr Gly
267      260      265      270
268 Ile Tyr Tyr Cys Trp Glu Glu Tyr Arg Val Leu Arg Asp Lys Gly Ala
269      275      280      285
270 Ser Ile Ser Gln Leu Gly Phe Thr Thr Asn Leu Ser Ala Tyr Gln Ser
271      290      295      300
272 Val Gln Glu Thr Trp Leu Ala Ala Leu Ile Val Leu Ala Val Leu Glu
273 305      310      315      320
274 Ala Ile Leu Leu Leu Met Leu Ile Phe Leu Arg Gln Arg Ile Arg Ile
275      325      330      335
276 Ala Ile Ala Leu Leu Lys Glu Ala Ser Lys Ala Val Gly Gln Met Met
277      340      345      350
278 Ser Thr Met Phe Tyr Pro Leu Val Thr Phe Val Leu Leu Leu Ile Cys
279      355      360      365
280 Ile Ala Tyr Trp Ala Met Thr Ala Leu Tyr Leu Ala Thr Ser Gly Gln
281      370      375      380
282 Pro Gln Tyr Val Leu Trp Ala Ser Asn Ile Ser Ser Pro Gly Cys Glu
283 385      390      395      400
284 Lys Val Pro Ile Asn Thr Ser Cys Asn Pro Thr Ala His Leu Val Asn
285      405      410      415
286 Ser Ser Cys Pro Gly Leu Met Cys Val Phe Gln Gly Tyr Ser Ser Lys
287      420      425      430
288 Gly Leu Ile Gln Arg Ser Val Phe Asn Leu Gln Ile Tyr Gly Val Leu
289      435      440      445
290 Gly Leu Phe Trp Thr Leu Asn Trp Val Leu Ala Leu Gly Gln Cys Val
291      450      455      460
292 Leu Ala Gly Ala Phe Ala Ser Phe Tyr Trp Ala Phe His Lys Pro Gln
293 465      470      475      480
294 Asp Ile Pro Thr Phe Pro Leu Ile Ser Ala Phe Ile Arg Thr Leu Arg
295      485      490      495
296 Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile Leu Thr Leu Val
297      500      505      510
298 Gln Ile Ala Arg Val Ile Leu Glu Tyr Ile Asp His Lys Leu Arg Gly
299      515      520      525

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